

## RACT-00100.ST25 SEQUENCE LISTING

<110>	McDan <sup>*</sup> Raush	ive Sur iel, St el, Fra James	even	S, L	td.									
<120>	Recom	Recombinant Organophosphorous Acid Anhydrase and Methods of Use												
<130>	TAMK1	TAMK145												
<140> <141>	US 08/252,384 1994-06-01													
<150> <151>	US 07/928,540 1992-08-13													
<150> <151>	US 07/344,258 1989-04-27													
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act ct	g ctc g u Leu d	gc ggc	ctg	gct	ggg	tgc	gcg	agc	gtg	gct	gga	tcg	atc	155
Thr Le	u Leu C	SIY GIY 20	Leu	Ala	Gly	Cys	A I a 25	Ser	Val	Ala	Gly	Ser 30	Ile	
ggc ac	a ggc g	gat cgg	atc	aat	acc	gtg	cgc	ggt	cct	atc	aça	atc	tct	203
Gly Th	r Giy A	Asp Arg 85	Ile	Asn	Thr	Va I 40	Arg	Gly	Pro	Ile	Thr 45	Ile	Ser.	
A22 C2	a aat t		cta	act	cac	gag	cac	atc	tgc	ggc	agc	tcg	gca	251
yaa yo	g ggr i	tc aca	ccg					_						
gaa gc Glu Al	a Gly F 50	he Thr	Leu	Thr	His 55	Ğlü	His	Ile	Cys	GTy 60	Ser	Ser	Ala	
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Glu Al gga tt	a Gly F 50 c ttg c e Leu A	he Thr gt gct	Leu tgg	Thr	His 55 gag	Glu	ttc	Ile	Cys	Gly 60 cqc	ser	ser	cta	299
gga tt Gly Ph 65 gcg ga	a Gly F 50 c ttg c e Leu A a aag g	the Thr tgt gct trg Ala	tgg Trp	Thr cca Pro 70 gga	His 55 gag Glu ttg	ttc Phe	ttc Phe cgc	ggt Gly gcc	agc ser 75	Gly 60 cgc Arg	ser aaa Lys gct	gct Ala ggc	cta Leu gtg	299 347
gga tt Gly Ph 65 gcg ga	a Gly F 50 c ttg c e Leu A	the Thr tgt gct trg Ala	tgg Trp	Thr cca Pro 70 gga	His 55 gag Glu ttg	ttc Phe	ttc Phe cgc	ggt Gly gcc	agc ser 75	Gly 60 cgc Arg	ser aaa Lys gct	gct Ala ggc	cta Leu gtg	
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						ttc Phe 150										539
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atc Ile	gac Asp	caa G1n 290	ggc Gly	tac Tyr	atg Met	aaa Lys	caa Gln 295	atc Ile	ctc Leu	gtt Val	tcg Ser	aat Asn 300	gac Asp	tgg Trp	ctg Leu	971
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gtg Val 320	aac Asn	ccc Pro	gac Asp	ggg Gly	atg Met 325	gcc Ala	ttc Phe	att Ile	cca Pro	ctg Leu 330	aga Arg	gtg val	atc Ile	cca Pro	ttc Phe 335	1067
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Thr	Asn	Pro	Ala	Arg	Phe	Leu	Ser	Pro	Thr	Leu	Arg	Ala	Ser
			355	_				360			•		365

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Ala Gly Phe Thr Leu Thr His Glu His Ile Cys Gly Ser Ser Ala Gly 50 60

Phe Leu Arg Ala Trp Pro Glu Phe Phe Gly Ser Arg Lys Ala Leu Ala 65 70 75 80

Glu Lys Ala Val Arg Gly Leu Arg Arg Ala Arg Ala Gly Val Arg 85 90 95

Thr Ile Val Asp Val Ser Thr Phe Asp Ile Gly Arg Asp Val Ser Leu 100 105 110

Leu Ala Glu Val Ser Arg Ala Ala Asp Val His Ile Val Ala Ala Thr 115 120 125

Gly Leu Trp Phe Asp Pro Pro Leu Ser Met Arg Leu Arg Ser Val Glu 130 135 140

Glu Leu Thr Gln Phe Phe Leu Arg Glu Ile Gln Tyr Gly Ile Glu Asp 145 150 155 160

Thr Gly Ile Arg Ala Gly Ile Ile Lys Val Ala Thr Thr Gly Lys Ala 165 170 175

Thr Pro Phe Gln Glu Leu Val Leu Lys Ala Ala Arg Ala Ser Leu 180 185 190

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Gly	Glu 210	Gln	Gln	Ala	Ala	Ile 215	Phe	Glu	Ser	Glu	Gly 220	Leu	Ser	Pro	Ser
Arg 225	val	Cys	Ile	Gly	His 230	Ser	Asp	Asp	Thr	Asp 235	Asp	Leu	Ser	Tyr	Leu 240
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His	Ser	Ala	11e 260	Gly	Leu	Glu	Asp	Asn 265	Ala	Ser	Ala	Ser	Ala 270	Leu	Leu
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G]y 305	Phe	Ser	Ser	Tyr	Val 310	Thr	Asn	Ile	Met	Asp 315	val	Met	Asp	Arg	va1 320
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Arg	Glu	Lys	Gly 340	Val	Pro	Gln	Glu	Thr 345	Leu	Ala	Gly	Ile	Thr 350	val	Thr
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